Fig.1.

```
          PstI
CAGGTGCAGCTGCAGGAGTCAGGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGAGACTC
 Q  V  Q  L  Q  E  S  G  G  G  L  V  Q  A  G  G  S  L  R  L

TCCTGTGCAGCCTCGGGACGCGCCACCAGTGGTCATGGTCACTATGGTATGGGCTGGTTC
 S  C  A  A  S  G  R  A  T  S  G  H  G  H  Y  G  M  G  W  F

CGCCAGGTTCCAGGGAAGGAGCGTGAGTTTGTCGCAGCTATTAGGTGGAGTGGTAAAGAG
 R  Q  V  P  G  K  E  R  E  F  V  A  A  I  R  W  S  G  K  E

ACATGGTATAAAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGATAACGCCAAGACT
 T  W  Y  K  D  S  V  K  G  R  F  T  I  S  R  D  N  A  K  T

ACGGTTTATCTGCAAATGAACAGCCTGAAACCTGAAGATACGGCCGTTTATTATTGTGCC
 T  V  Y  L  Q  M  N  S  L  K  P  E  D  T  A  V  Y  Y  C  A

GCTCGACCGGTCCGCGTGGATGATATTTCCCTGCCGGTTGGGTTTGACTACTGGGGCCAG
 A  R  P  V  R  V  D  D  I  S  L  P  V  G  F  D  Y  W  G  Q

GGGACCCAGGTCACCGTCTCCTCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAA
 G  T  Q  V  T  V  S  S  E  Q  K  L  I  S  E  E  D  L  N

TAAGGGCTAAGCTCGAATTC
              EcoRI
```

Fig.2A.

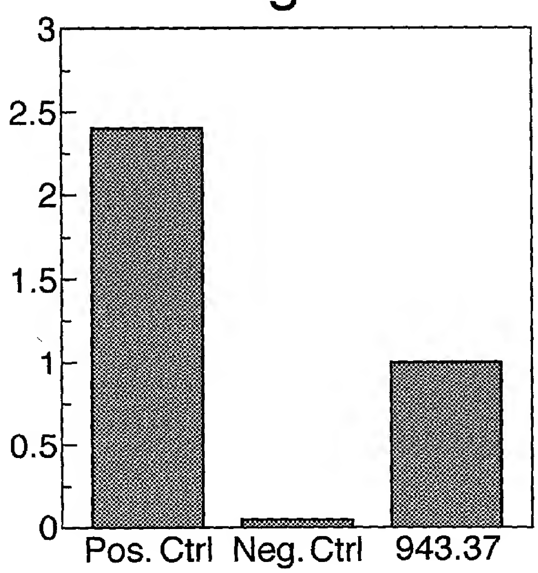
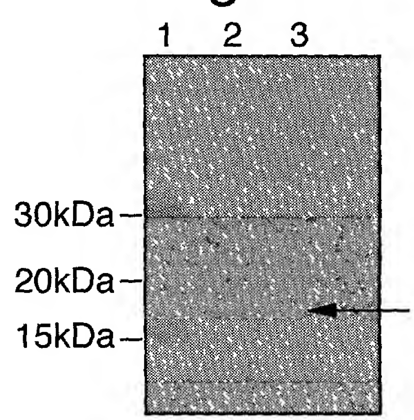


Fig.2B.



1: Molecular Weight Markers
2: 943.37 Sample
3: Neg. Ctrl

Fig.3A.

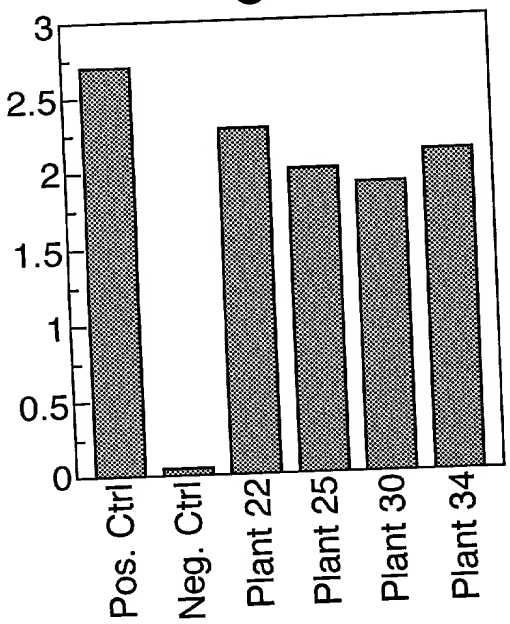
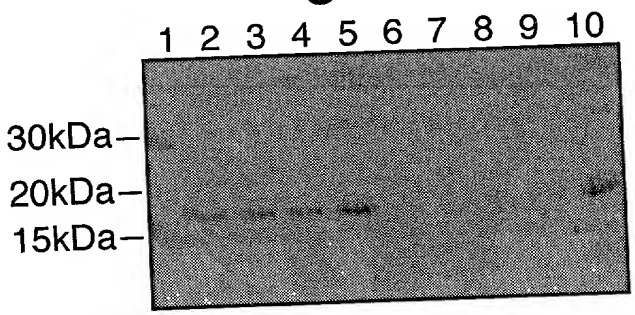
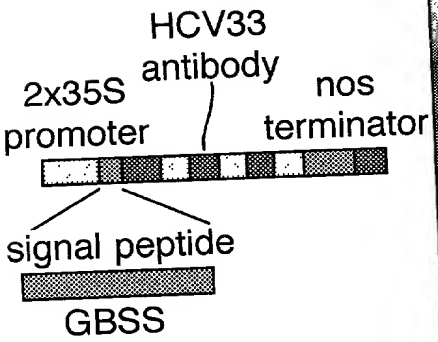


Fig.3B.



1: Molecular Weight Markers
2-5: Samples Plant.22, 25, 30,34
6-9: Neg. Plants Samples
10: Positive Ctrl (P.pastoris produced)

Fig.4.



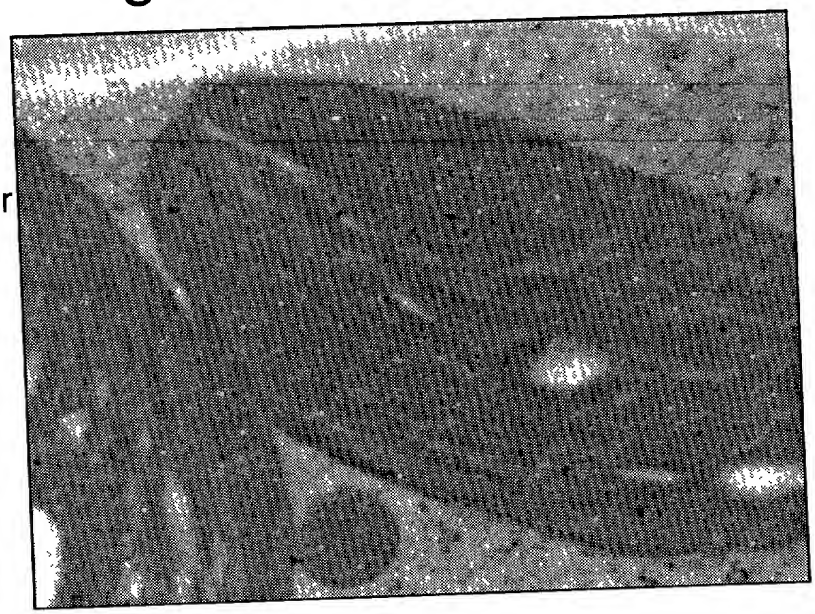


Fig.5.

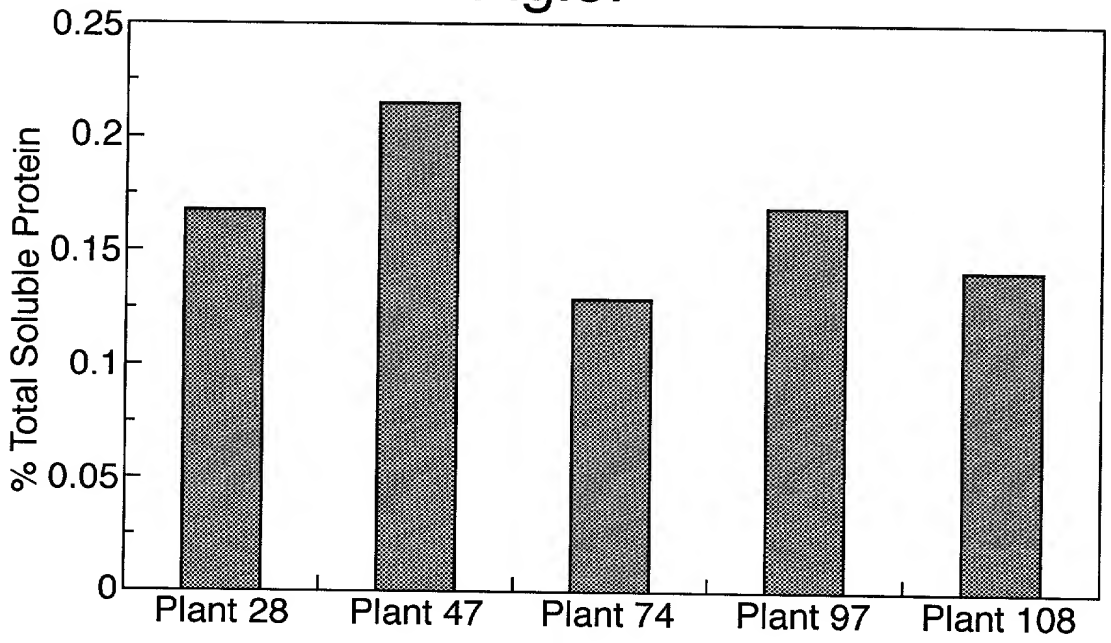


Fig.6.

PstI

CAGGTGCAG**CTGCAG**CAGTCAGGGGGAGGCTTGGTGCAGGCTGGGGGGTCTCTGAGACTC
Q V Q L Q Q S G G G L V Q A G G S L R L

TCCTGTGTAGCTTCTGAAAGCAGCTTCAGCAACAATCACATGGGCTGGTACCGCCGGGCT
S C V A S E S S F S N N H M G W Y R R A

CCAGGGAACCAGCGCGAGCTGGTCGCAACTATTAGTCCTGGTGGTAGCACACACTATGTA
P G N Q R E L V A T I S P G G S T H Y V

GACTCCGTGAAGGGCCGATTCACCATCTCCCGAGACAACGCCAAGAACACAGTGTATCTA
D S V K G R F T I S R D N A K N T V Y L

CAAATGGACAGCCTGAAACCAGAGGACACGGCCGTCTATTACTGTGCTGCCAAGGGGAGG
Q M D S L K P E D T A V Y Y C A A K G R

PstI

GGG**CTGCAG**GCTATGCAGTACTGGGGCCAGGGGACCCTGGTCACCGTCTCCTCAGCGCAC
G L Q A M Q Y W G Q G T L V T V S S A H

CACAGCGAAGACCCCAGCTCCGCGGCCGCCCATCACCATCACCATCACGGGGCCGCAGAA
H S E D P S S A A A H H H H H H G A A E

CAAAAACTCATCTCAGAAGAGGATCTGAATGGGGCCGCATAGTAA**CAATTG**
Q K L I S E E D L N G A A MunI

Fig.7.

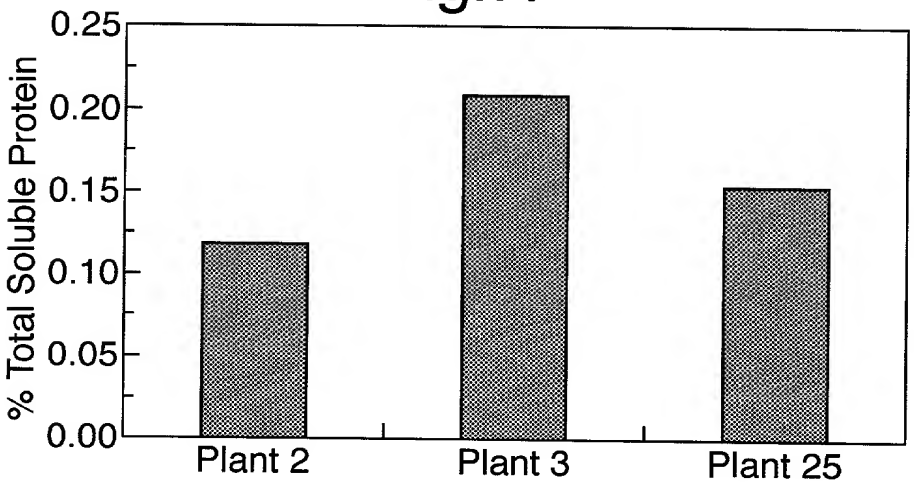
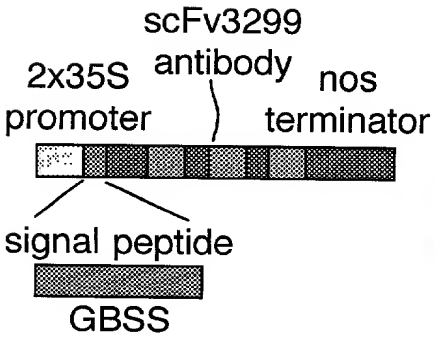

0.25
0.20
0.15
0.10
0.05
0.00
% Total Soluble Protein
Plant 2
Plant 3
Plant 25

Fig.8.


scFv3299
antibody
2x35S
promoter
nos
terminator
signal peptide
GBSS

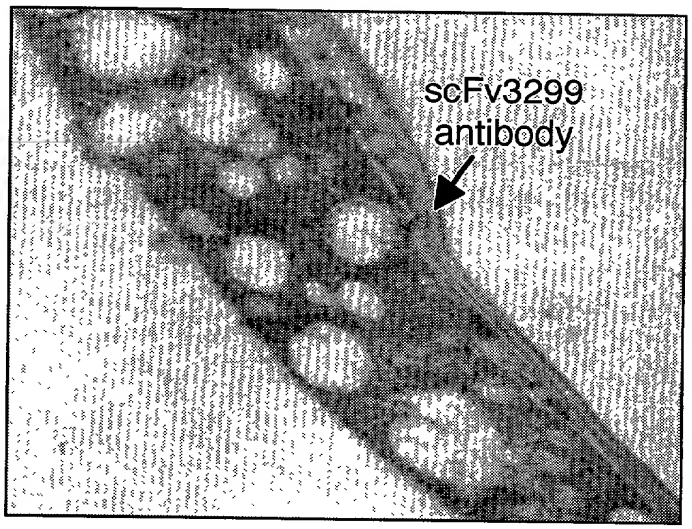

scFv3299
antibody

Fig.9.

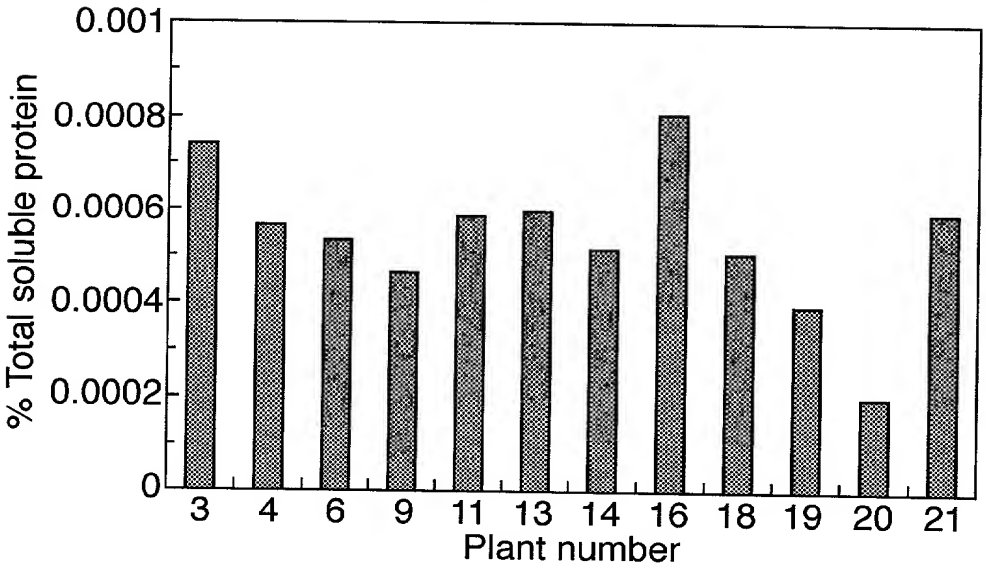

0.001
0.0008
0.0006
0.0004
0.0002
0
% Total soluble protein
3
4
6
9
11
13
14
16
18
19
20
21
Plant number

Fig.10A.

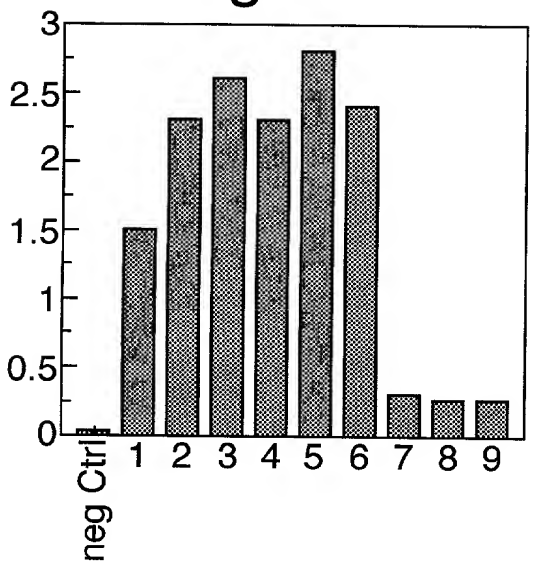
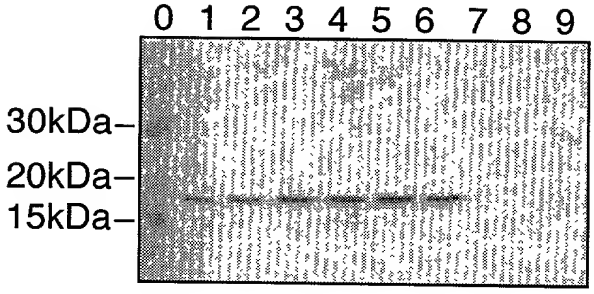
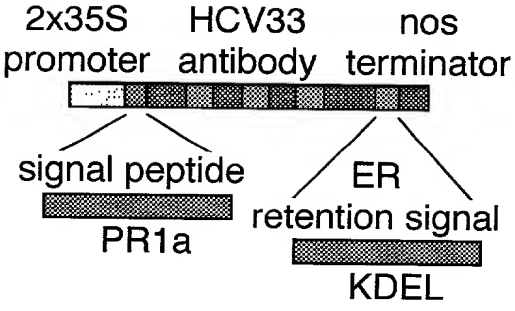


Fig.10B.



0: Molecular Weight Markers
1-6: pPV.8-PRIa-HCV33-myc-SKDEL plants
7-9: pPV.8-GBSS-HCV33-myc-SKDEL plants

Fig.11.



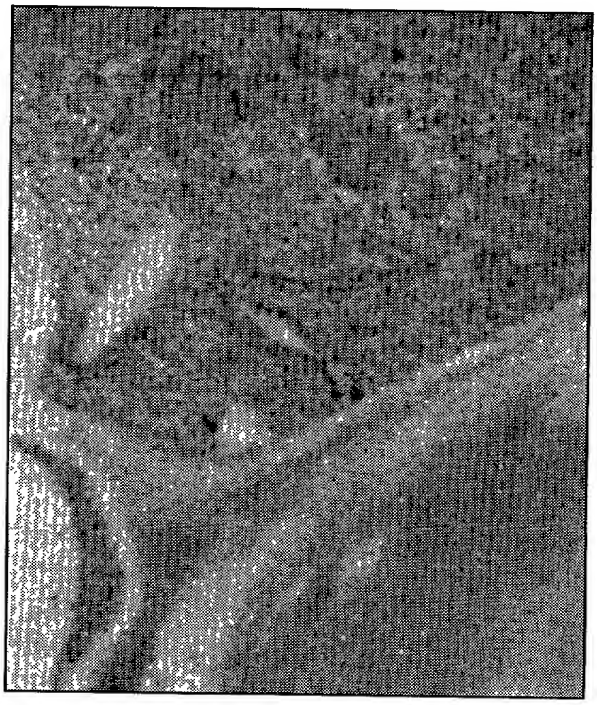


Fig.12.

PstI

CAGGTGCAG**CTGCAG**GAGTCTGGGGGAGGCCTGGTGCAGGCTGGGGGGTCTCTGAGACTC
Q V Q L Q E S G G G L V Q A G G S L R L

TCCTGTGTAGCCTCTGGAAACACCTTCAGTATCATAGCTATGGCCTGGTACCGCCAGGCT
S C V A S G N T F S I I A M A W Y R Q A

CCAGGGAAGCAGCGCGAGGTGGTCGCAAGTATTAATAGTATTGGCAGCACAAATTATGCA
P G K Q R E V V A S I N S I G S T N Y A

GACTCCGTGAAGGGGCGATTCACCATCTCCAGAGACAACGCCAAGAACACAGTGTATCTG
D S V K G R F T I S R D N A K N T V Y L

CAAATGAGCAGCCTGAAACCTGAGGACACGGCCGTCTATTACTGTGCTGCCGGTAATTTG
Q M S S L K P E D T A V Y Y C A A G N L

CTGGTTAAGAGGCCTTACTGGGGCCAGGGGACCCTGGTCACCGTCTCCTCAGAACCCAAG
L V K R P Y W G Q G T L V T V S S E P K

ACACCAAAACCACAACCAGCGGCCGCCCATCACCATCACCATCACGGGGCCGCAGAACAA
T P K P Q P A A A H H H H H H G A A E Q

AAACTCATCTCAGAAGAGGATCTGAATGGGGCCGCATAGTAA**CAATTG**
K L I S E E D L N G A A *MunI*

Fig.13.

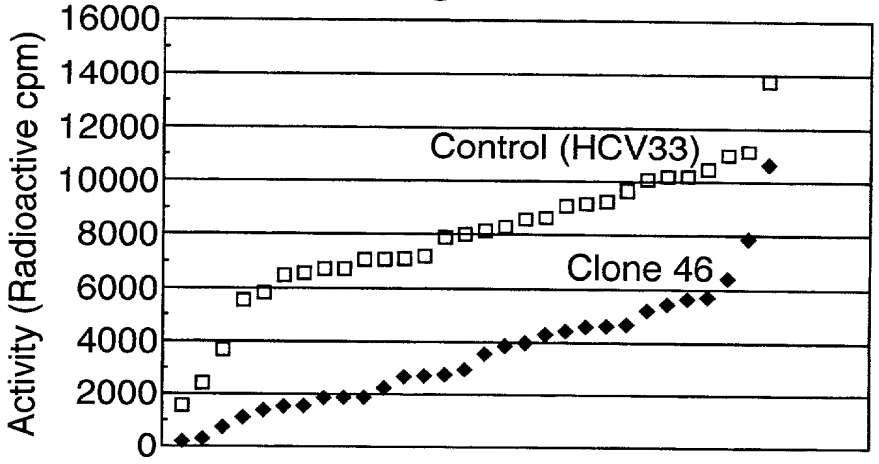


Fig.14.

```
  NcoI                PstI
ACCATGGCCCAGGTGAAACTGCAGCAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCCCT
 T  M  A  Q  V  K  L  Q  Q  S  G  G  G  L  V  Q  A  G  G  P

CTGAGGCTCTCCTGTGCAGCCTCTGGACGCACCTTCAGTAACTATGCCGTGGGCTGGTTC
 L  R  L  S  C  A  A  S  G  R  T  F  S  N  Y  A  V  G  W  F

CGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTCGCTGCTATTAGCCGTGATGGTGGGCGC
 R  Q  A  P  G  K  E  R  E  F  V  A  A  I  S  R  D  G  G  R

ACATACTATGCGGACTCCGTGAAGGGCCGATTCGCCGTCTCCAGAGACTACGCCGAGAAC
 T  Y  Y  A  D  S  V  K  G  R  F  A  V  S  R  D  Y  A  E  N

ACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTAAC
 T  V  Y  L  Q  M  N  S  L  K  P  E  D  T  A  V  Y  Y  C  N

ACAAGGGCCTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAGCGCACCACAGCGAA
 T  R  A  Y  W  G  Q  G  T  Q  V  T  V  S  S  A  H  H  S  E

GACCCCAGCTCCGCGGCCGCCCATCACCATCACCATCACGGGGCCGCAGAACAAAAACTC
 D  P  S  S  A  A  A  H  H  H  H  H  H  G  A  A  E  Q  K  L

ATCTCAGAAGAGGATCTGAATGGGGCCGCATAGTAACAATTG
 I  S  E  E  D  L  N  G  A  A        MunI
```

Fig.15.

```
  NcoI                PstI
ACCATGGCCCAGGTGAAACTGCAGCAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCCCT
 T  M  A  Q  V  K  L  Q  Q  S  G  G  G  L  V  Q  A  G  G  P

CTGAGGCTCTCCTGTGCAGCCTCTGGACGCACCTTCAGTAACTATGCCGTGGGCTGGTTC
 L  R  L  S  C  A  A  S  G  R  T  F  S  N  Y  A  V  G  W  F

CGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTCGCTGCTATTAGCCGTGATGGTGGGCGC
 R  Q  A  P  G  K  E  R  E  F  V  A  A  I  S  R  D  G  G  R

ACATACTATGCGGACTCCGTGAAGGGCCGATTCGCCGTCTCCAGAGACTACGCCGAGAAC
 T  Y  Y  A  D  S  V  K  G  R  F  A  V  S  R  D  Y  A  E  N

ACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTAAC
 T  V  Y  L  Q  M  N  S  L  K  P  E  D  T  A  V  Y  Y  C  N

ACAAGGGCCTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAGCGCACCACAGCGAA
 T  R  A  Y  W  G  Q  G  T  Q  V  T  V  S  S  A  H  H  S  E

GACCCCAGCTCCGCGGCCGCCCATCACCATCACCATCACGGGGCCGCAGAACAAAAACTC
 D  P  S  S  A  A  A  H  H  H  H  H  H  G  A  A  E  Q  K  L

ATCTCAGAAGAGGATCTGAATTCTGAGAAAGATGAGCTATGACAATTG
 I  S  E  E  D  L  N  S  E  K  D  E  L        MunI
```

Fig.16.

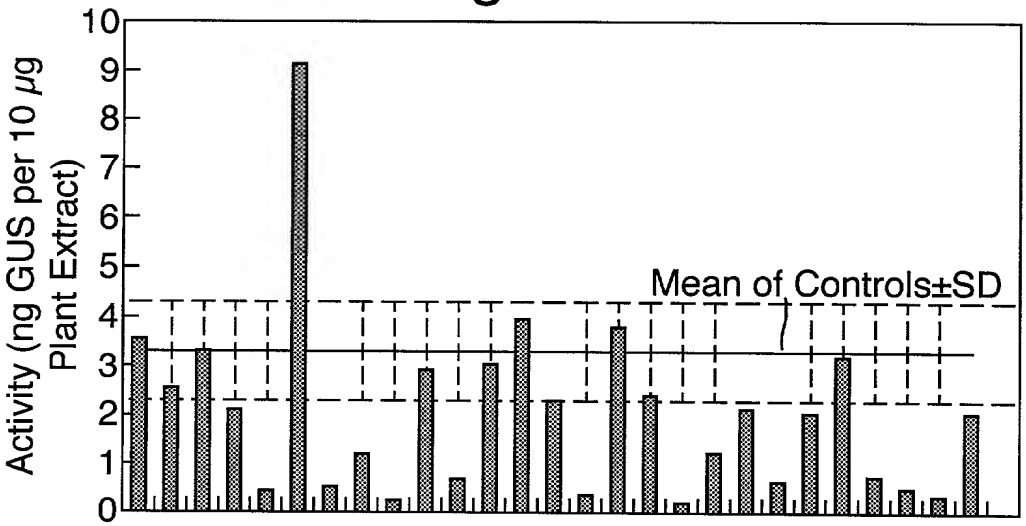


Fig.17A.

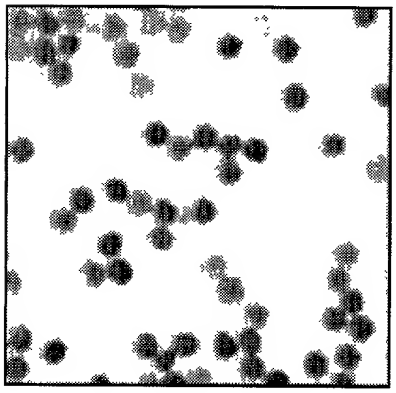


Fig.17B.

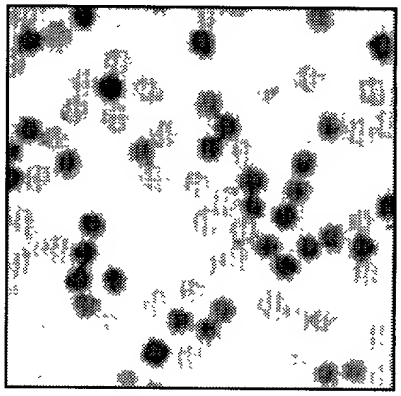


Fig.18.

```
      NcoI          PstI
      ------        ------
 1    ccatggaggt gcagctgcag gagtcagggg gaggattggt gcaggctggg
        >>.....................HCV33.....................>
          m  e  v  q  l  q  e  s  g  g  g  l  v  q  a  g

51    ggctctctga gactctcctg tgcagcctcg ggacgcgcca ccagtggtca
      >.....................HCV33.....................>
        g  s  l  r  l  s  c  a  a  s  g  r  a  t  s  g

101   tggtcactat ggtatgggct ggttccgcca ggttccaggg aaggagcgtg
      >.....................HCV33.....................>
      h  g  h  y  g  m  g  w  f  r  q  v  p  g  k  e  r

151   agtttgtcgc agctattagg tggagtggta aagagacatg gtataaagac
      >.....................HCV33.....................>
       e  f  v  a  a  i  r  w  s  g  k  e  t  w  y  k  d

201   tccgtgaagg gccgattcac catctccaga gataacgcca agactacggt
      >.....................HCV33.....................>
        s  v  k  g  r  f  t  i  s  r  d  n  a  k  t  t

251   ttatctgcaa atgaacagcc tgaaacctga agatacggcc gtttattatt
      >.....................HCV33.....................>
      v  y  l  q  m  n  s  l  k  p  e  d  t  a  v  y  y

301   gtgccgctcg accggtccgc gtggatgata tttccctgcc ggttgggttt
      >.....................HCV33.....................>
       c  a  a  r  p  v  r  v  d  d  i  s  l  p  v  g  f
                             BstEII
                             -------
351   gactactggg gccaggggac ccaggtcacc gtctcctcag aacccaagac
      >................HCV33.............>>>>..Hinge..>
        d  y  w  g  q  g  t  q  v  t  v  s  s  e  p  k

401   accaaaacca caaccacaac cacaaccaca accacaaccc aatcctacaa
      >.....................Hinge.....................>
      t  p  k  p  q  p  q  p  q  p  q  p  q  p  n  p  t

451   cagaatccaa gtgtcccaaa tgtccagccc ctgagctcct gggagggccc
      >.........Hinge.........>>>>.........CH2.........>
       t  e  s  k  c  p  k  c  p  a  p  e  l  l  g  g  p

501   tcagtcttca tcttcccccc gaaacccaag gacgtcctct ccatttctgg
      >.....................CH2.....................>
        s  v  f  i  f  p  p  k  p  k  d  v  l  s  i  s

551   gaggcccgag gtcacgtgcg ttgtggtaga cgtgggccag gaagaccccg
      >.....................CH2.....................>
      g  r  p  e  v  t  c  v  v  v  d  v  g  q  e  d  p

601   aggtcagttt caactggtac attgatggcg cagaggtgcg aacggccaac
      >.....................CH2.....................>
       e  v  s  f  n  w  y  i  d  g  a  e  v  r  t  a  n

651   acgaggccaa aagaggaaca gttcaacagc acgtaccgcg tggtcagcgt
      >.....................CH2.....................>
```

Fig.18 (Cont).

```
          t  r  p  k  e  e  q  f  n  s  t  y  r  v  v  s

701  cctgcccatc cagcaccagg actggctgac ggggaaagag ttcaaatgca
     >.......................CH2........................>
     v  l  p  i  q  h  q  d  w  l  t  g  k  e  f  k  c
       HincII
       ------
751  aggtcaacaa caaagctctc ccggccccca tcgagaagac catctccaag
     >.......................CH2........................>
      k  v  n  n  k  a  l  p  a  p  i  e  k  t  i  s  k

801  gccaaagggc agacccggga gccgcaggtg tacgccctgg ccccacaccg
     >...>>>>.....................CH3.....................>
       a  k  g  q  t  r  e  p  q  v  y  a  l  a  p  h

851  ggaagagctg gccaaggaca ccgtgagcgt aacctgcctg gtcaaaggct
     >.......................CH3........................>
     r  e  e  l  a  k  d  t  v  s  v  t  c  l  v  k  g

901  tctacccacc tgatatcaac gttgagtggc agaggaacgg tcagccggag
     >.......................CH3........................>
      f  y  p  p  d  i  n  v  e  w  q  r  n  g  q  p  e

951  tcagagggca cctacgccac cacgccaccc cagctggaca acgacgggac
     >.......................CH3........................>

       s  e  g  t  y  a  t  t  p  p  q  l  d  n  d  g

1001 ctacttcctc tacagcaagc tctcggtggg aaagaacacg tggcagcggg
     >.......................CH3........................>
     t  y  f  l  y  s  k  l  s  v  g  k  n  t  w  q  r

1051 gagaaacctt cacctgtgtg gtgatgcacg aggccctgca caaccactac
     >.......................CH3........................>
      g  e  t  f  t  c  v  v  m  h  e  a  l  h  n  h  y
                                                EcoRI
                                                -------
1101 acccagaaat ccatcaccca gtcttcgggt aaataataag aattcgagct
     >..............CH3..............>>
       t  q  k  s  i  t  q  s  s  g  k

1151 cgaa
```

Fig.19.

```
        NcoI            PstI
       ------          ------
  1    ccatggaggt gcagctgcag gagtcagggg gaggattggt gcaggctggg
        >>....................HCV33......................>
          m  e   v  q  l  q   e  s  g   g  g  l   v  q  a  g

 51    ggctctctga gactctcctg tgcagcctcg ggacgcgcca ccagtggtca
       >......................HCV33......................>
        g  s  l   r  l  s   c  a  a  s   g  r  a   t  s  g

101    tggtcactat ggtatgggct ggttccgcca ggttccaggg aaggagcgtg
       >......................HCV33......................>
       h  g  h  y   g  m  g   w  f  r   q  v  p  g   k  e  r

151    agtttgtcgc agctattagg tggagtggta aagagacatg gtataaagac
       >......................HCV33......................>
        e  f  v   a  a  i  r   w  s  g   k  e  t   w  y  k  d

201    tccgtgaagg gccgattcac catctccaga gataacgcca agactacggt
       >......................HCV33......................>
        s  v  k   g  r  f   t  i  s  r   d  n  a   k  t  t

251    ttatctgcaa atgaacagcc tgaaacctga agatacggcc gtttattatt
       >......................HCV33......................>
       v  y  l  q   m  n  s   l  k  p   e  d  t  a   v  y  y

301    gtgccgctcg accggtccgc gtggatgata tttccctgcc ggttgggttt
       >......................HCV33......................>
        c  a  a   r  p  v  r   v  d  d   i  s  l   p  v  g  f
                                BstEII
                               -------
351    gactactggg gccaggggac ccaggtcacc gtctcctcag aacccaagac
       >................HCV33.................>>>>..Hinge..>
        d  y  w   g  q  g   t  q  v  t   v  s  s   e  p  k

401    accaaaacca caaccacaac cacaaccaca accacaaccc aatcctacaa
       >......................Hinge......................>
       t  p  k  p   q  p  q   p  q  p   q  p  q  p   n  p  t

451    cagaatccaa gtgtcccaaa tgtccagccc ctgagctcct gggagggccc
       >..........Hinge..........>>>>.........CH2..........>
        t  e  s   k  c  p  k   c  p  a   p  e  l   l  g  g  p

501    tcagtcttca tcttcccccc gaaacccaag gacgtcctct ccatttctgg
       >......................CH2........................>
        s  v  f   i  f  p   p  k  p  k   d  v  l   s  i  s

551    gaggcccgag gtcacgtgcg ttgtggtaga cgtgggccag gaagaccccg
       >......................CH2........................>
       g  r  p  e   v  t  c   v  v  v   d  v  g  q   e  d  p

601    aggtcagttt caactggtac attgatggcg cagaggtgcg aacggccaac
       >......................CH2........................>
        e  v  s   f  n  w  y   i  d  g   a  e  v   r  t  a  n

651    acgaggccaa aagaggaaca gttcaacagc acgtaccgcg tggtcagcgt
       >......................CH2........................>
```

Fig.19 (Cont).

```
        t  r  p  k  e  e  q  f  n  s  t  y  r  v  v  s

701  cctgcccatc cagcaccagg actggctgac ggggaaagag ttcaaatgca
     >.....................CH2.....................>
     v  l  p  i  q  h  q  d  w  l  t  g  k  e  f  k  c
       HincII
       ------
751  aggtcaacaa caaagctctc ccggccccca tcgagaagac catctccaag
     >.....................CH2.....................>
      k  v  n  n  k  a  l  p  a  p  i  e  k  t  i  s  k

801  gccaaagggc agacccggga gccgcaggtg tacgccctgg ccccacaccg
     >...>>>>.................CH3.....................>
       a  k  g  q  t  r  e  p  q  v  y  a  l  a  p  h

851  ggaagagctg gccaaggaca ccgtgagcgt aacctgcctg gtcaaaggct
     >.....................CH3.....................>
     r  e  e  l  a  k  d  t  v  s  v  t  c  l  v  k  g

901  tctacccacc tgatatcaac gttgagtggc agaggaacgg tcagccggag
     >.....................CH3.....................>
      f  y  p  p  d  i  n  v  e  w  q  r  n  g  q  p  e

951  tcagagggca cctacgccac cacgccaccc cagctggaca acgacgggac
     >.....................CH3.....................>

       s  e  g  t  y  a  t  t  p  p  q  l  d  n  d  g

1001 ctacttcctc tacagcaagc tctcggtggg aaagaacacg tggcagcggg
     >.....................CH3.....................>
     t  y  f  l  y  s  k  l  s  v  g  k  n  t  w  q  r

1051 gagaaacctt cacctgtgtg gtgatgcacg aggccctgca caaccactac
     >.....................CH3.....................>
      g  e  t  f  t  c  v  v  m  h  e  a  l  h  n  h  y

1101 acccagaaat ccatcaccca gtcttcgggt aaatctgaga aagatgagct
     >.............CH3.............>>>>.....SEKDEL.....>
       t  q  k  s  i  t  q  s  s  g  k  s  e  k  d  e
             EcoRI
            -------
1151 ataataagaa ttcgagctcg aa
     >
     |
```

Fig.20.

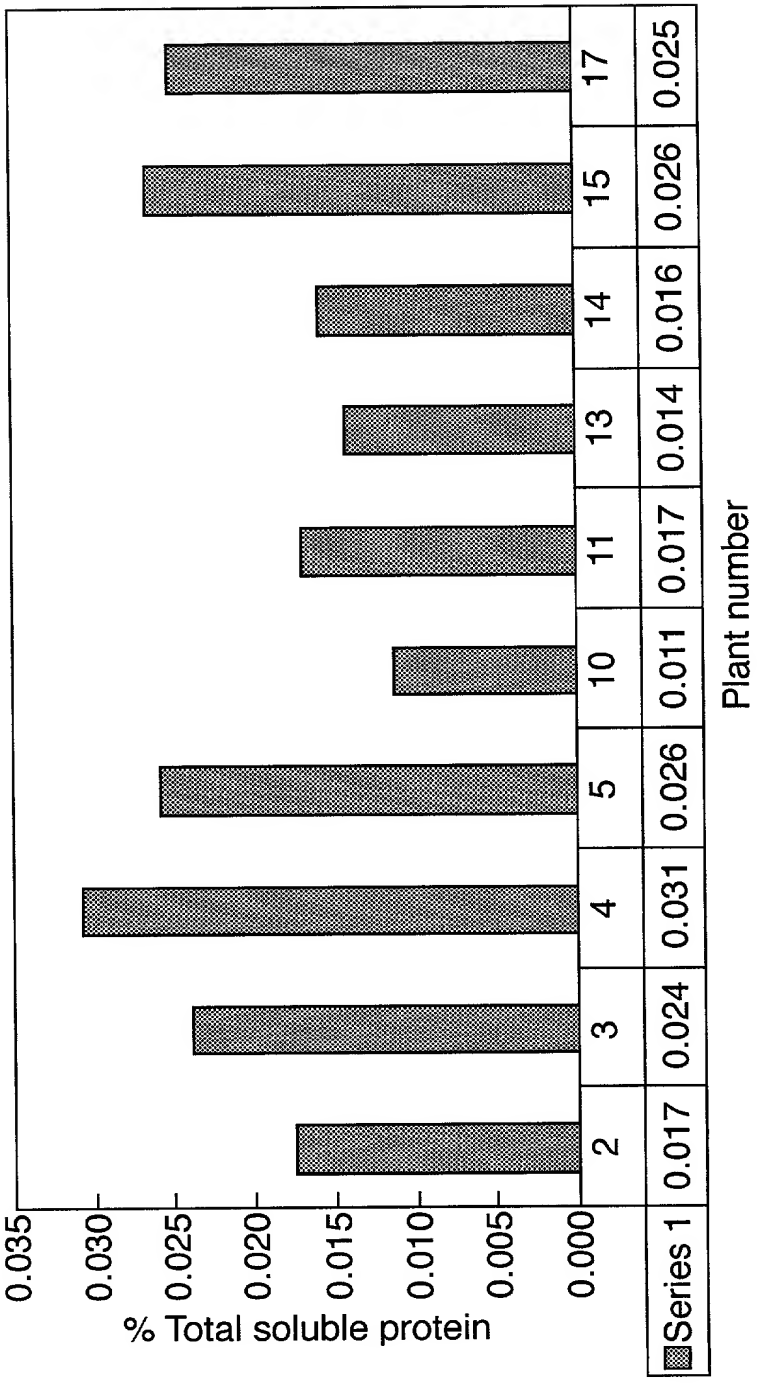
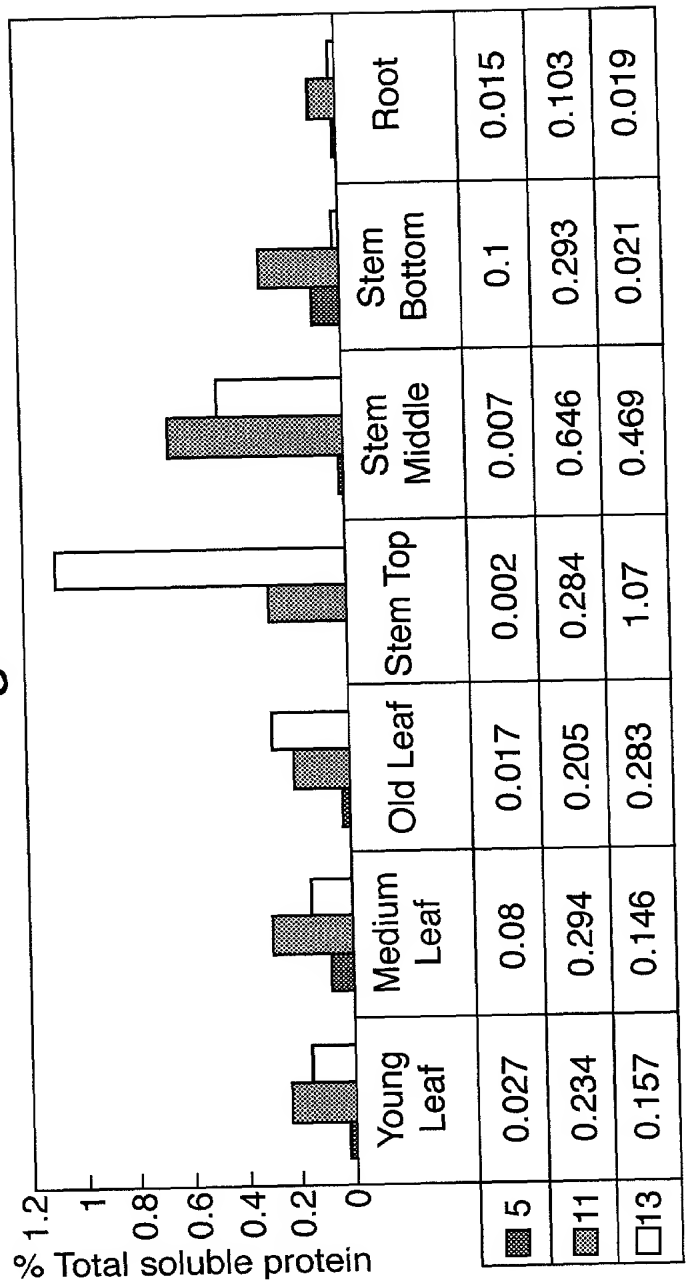

0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
% Total soluble protein
Series 1
0.017
0.024
0.031
0.026
0.011
0.017
0.014
0.016
0.026
0.025
2
3
4
5
10
11
13
14
15
17
Plant number

Fig.21.



	Young Leaf	Medium Leaf	Old Leaf	Stem Top	Stem Middle	Stem Bottom	Root
5	0.027	0.08	0.017	0.002	0.007	0.1	0.015
11	0.234	0.294	0.205	0.284	0.646	0.293	0.103
13	0.157	0.146	0.283	1.07	0.469	0.021	0.019

Fig.22.

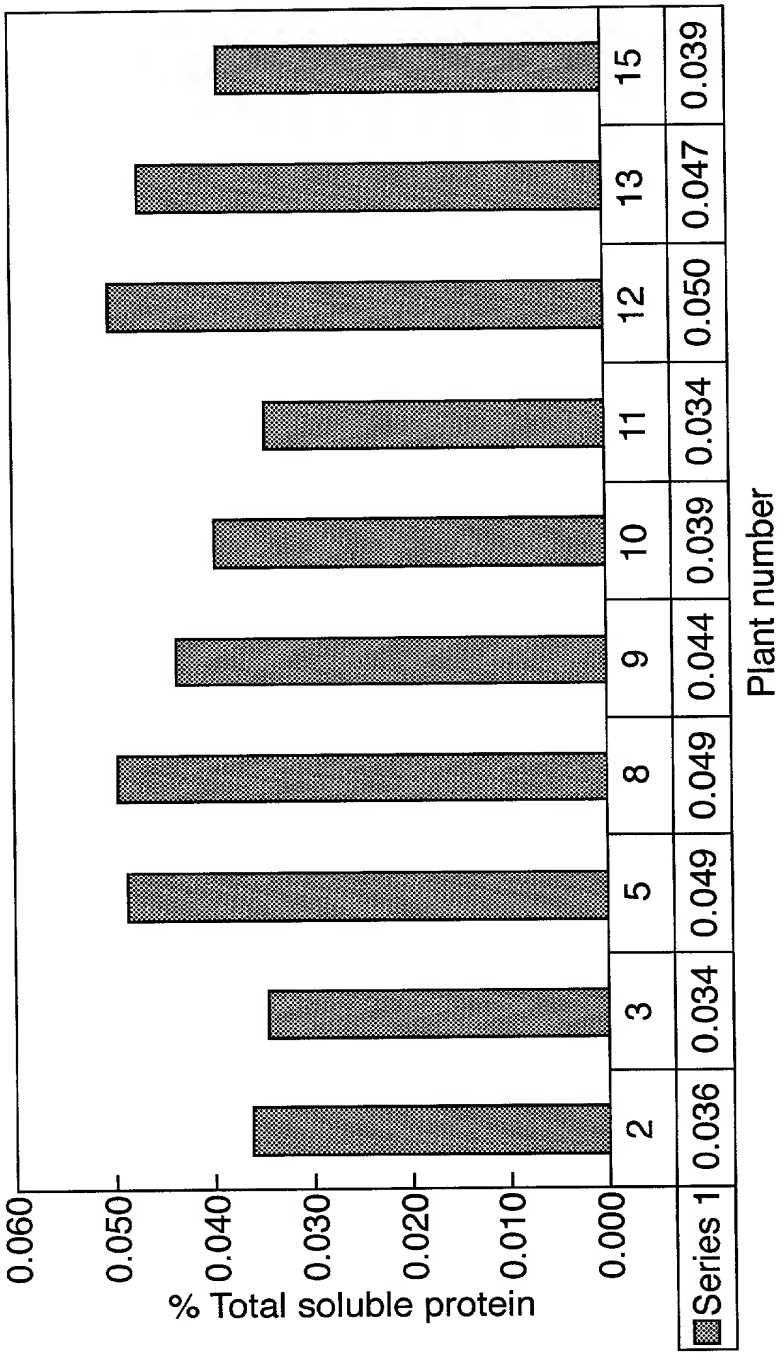
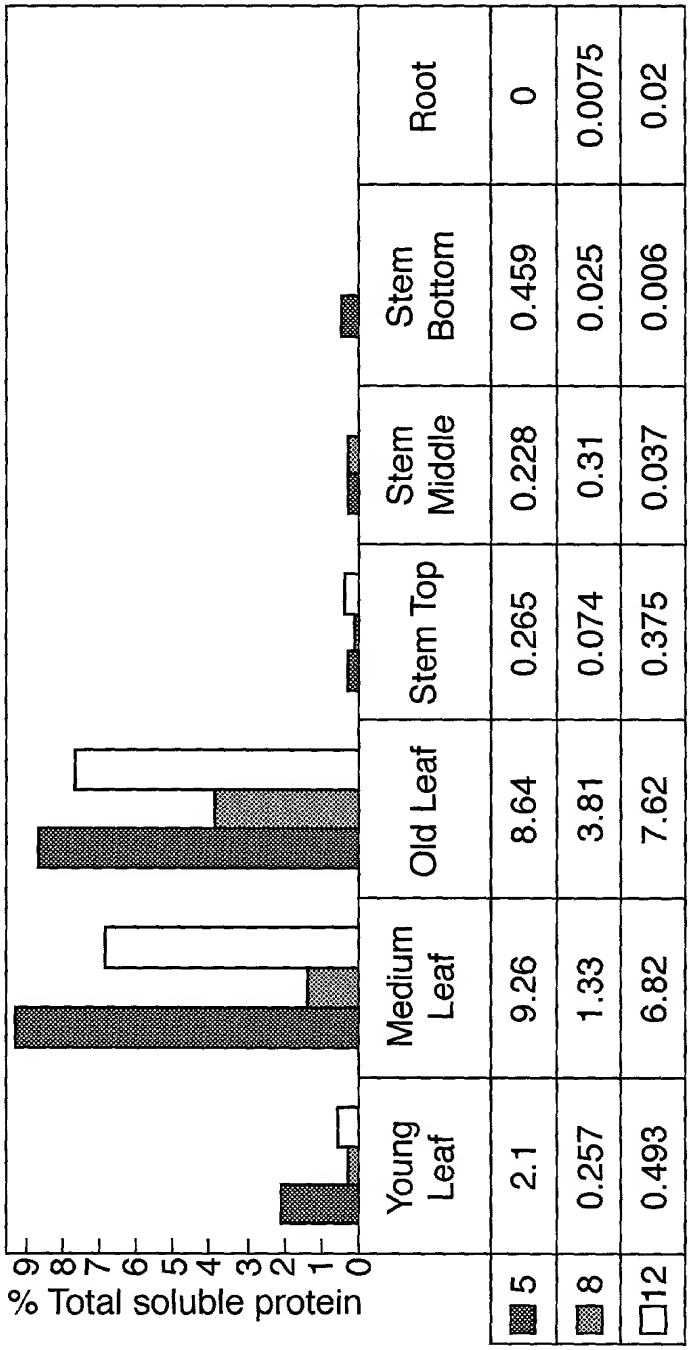

0.060
0.050
0.040
0.030
0.020
0.010
0.000
% Total soluble protein
2
3
5
8
9
10
11
12
13
15
Series 1
0.036
0.034
0.049
0.049
0.044
0.039
0.034
0.050
0.047
0.039
Plant number

Fig.23.



	Young Leaf	Medium Leaf	Old Leaf	Stem Top	Stem Middle	Stem Bottom	Root
5	2.1	9.26	8.64	0.265	0.228	0.459	0
8	0.257	1.33	3.81	0.074	0.31	0.025	0.0075
12	0.493	6.82	7.62	0.375	0.037	0.006	0.02

Fig.24.

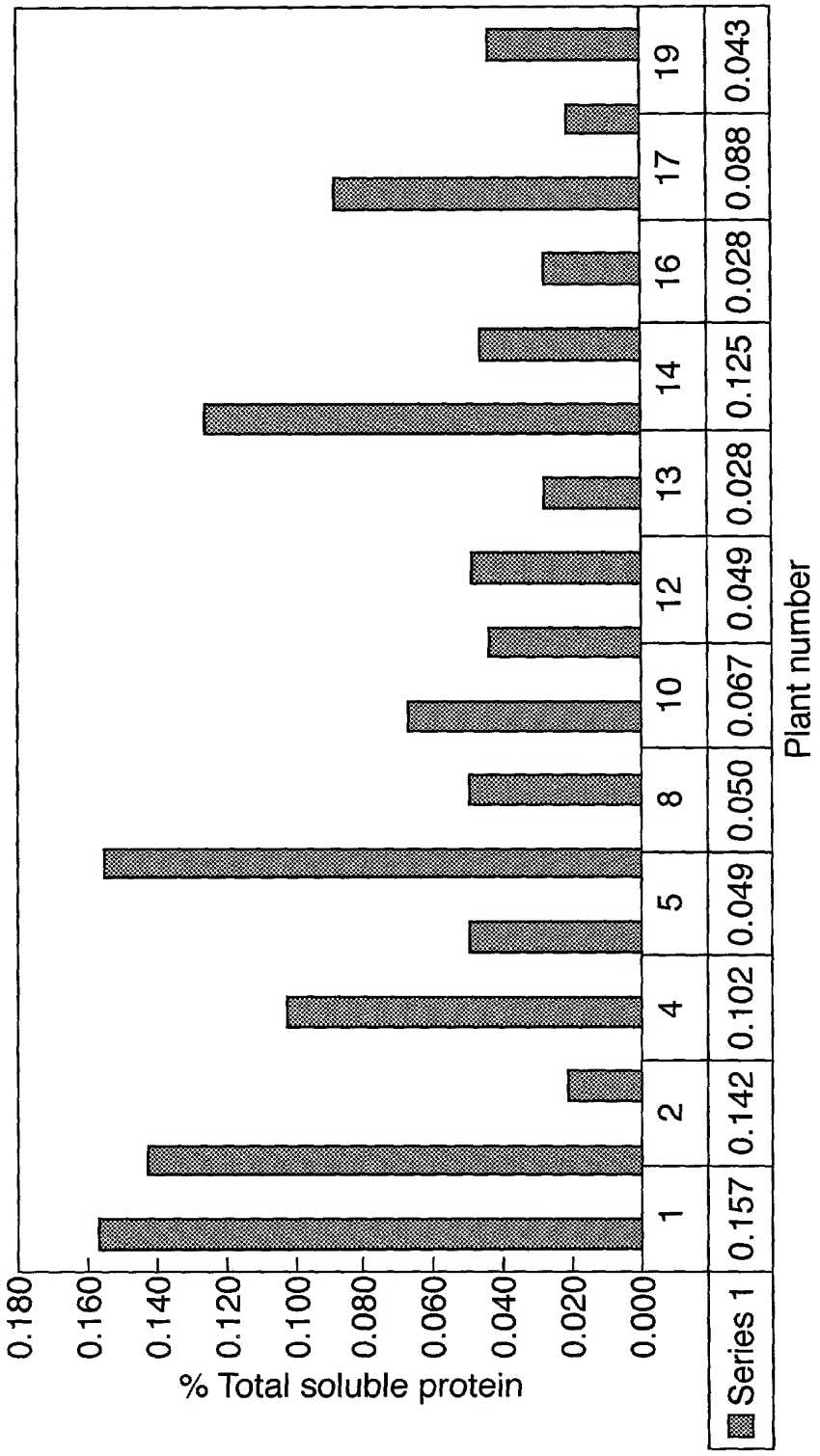
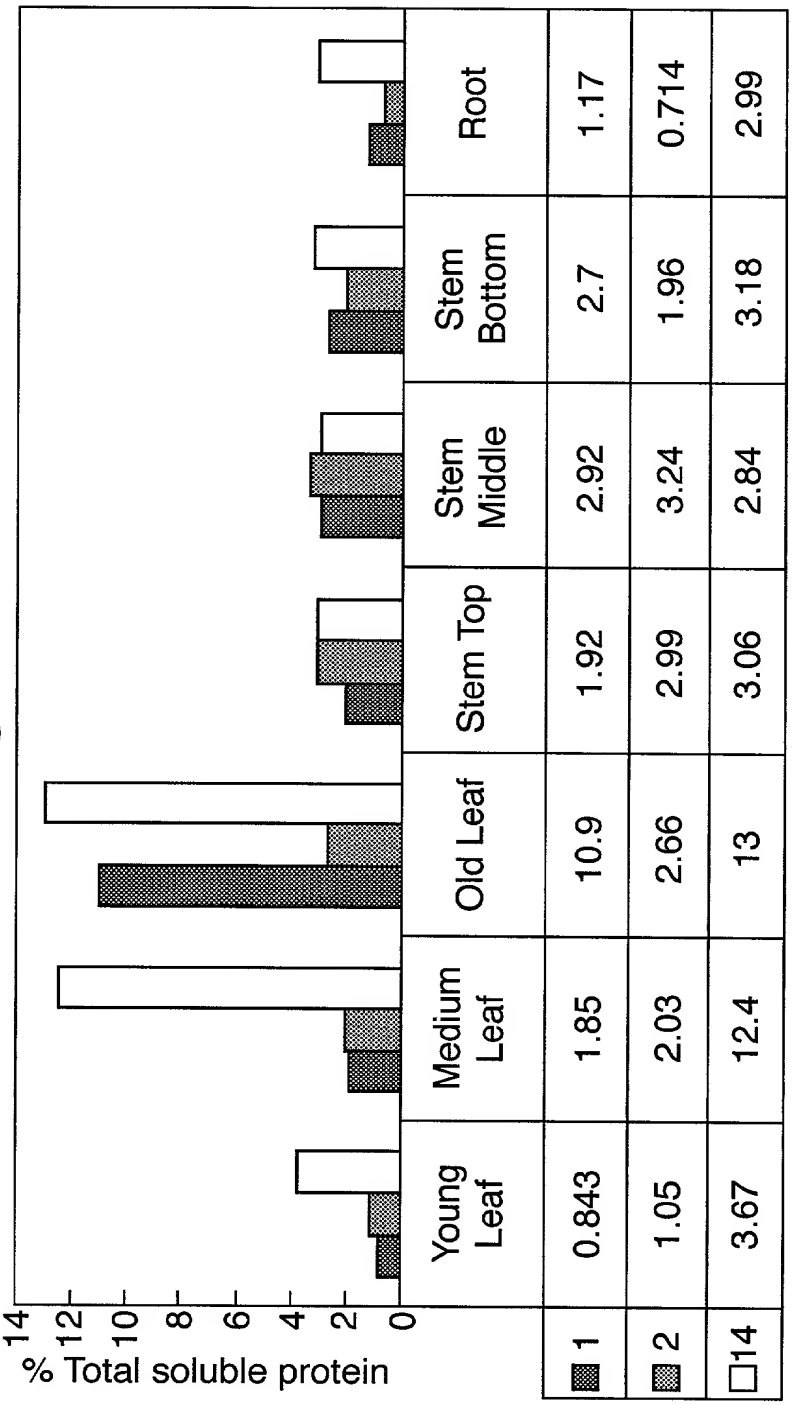

0.180
0.160
0.140
0.120
0.100
0.080
0.060
0.040
0.020
0.000
% Total soluble protein
1 2 4 5 8 10 12 13 14 16 17 19
Series 1 0.157 0.142 0.102 0.049 0.050 0.067 0.049 0.028 0.125 0.028 0.088 0.043
Plant number

Fig.25.



	Young Leaf	Medium Leaf	Old Leaf	Stem Top	Stem Middle	Stem Bottom	Root
1	0.843	1.85	10.9	1.92	2.92	2.7	1.17
2	1.05	2.03	2.66	2.99	3.24	1.96	0.714
14	3.67	12.4	13	3.06	2.84	3.18	2.99

Fig.26.

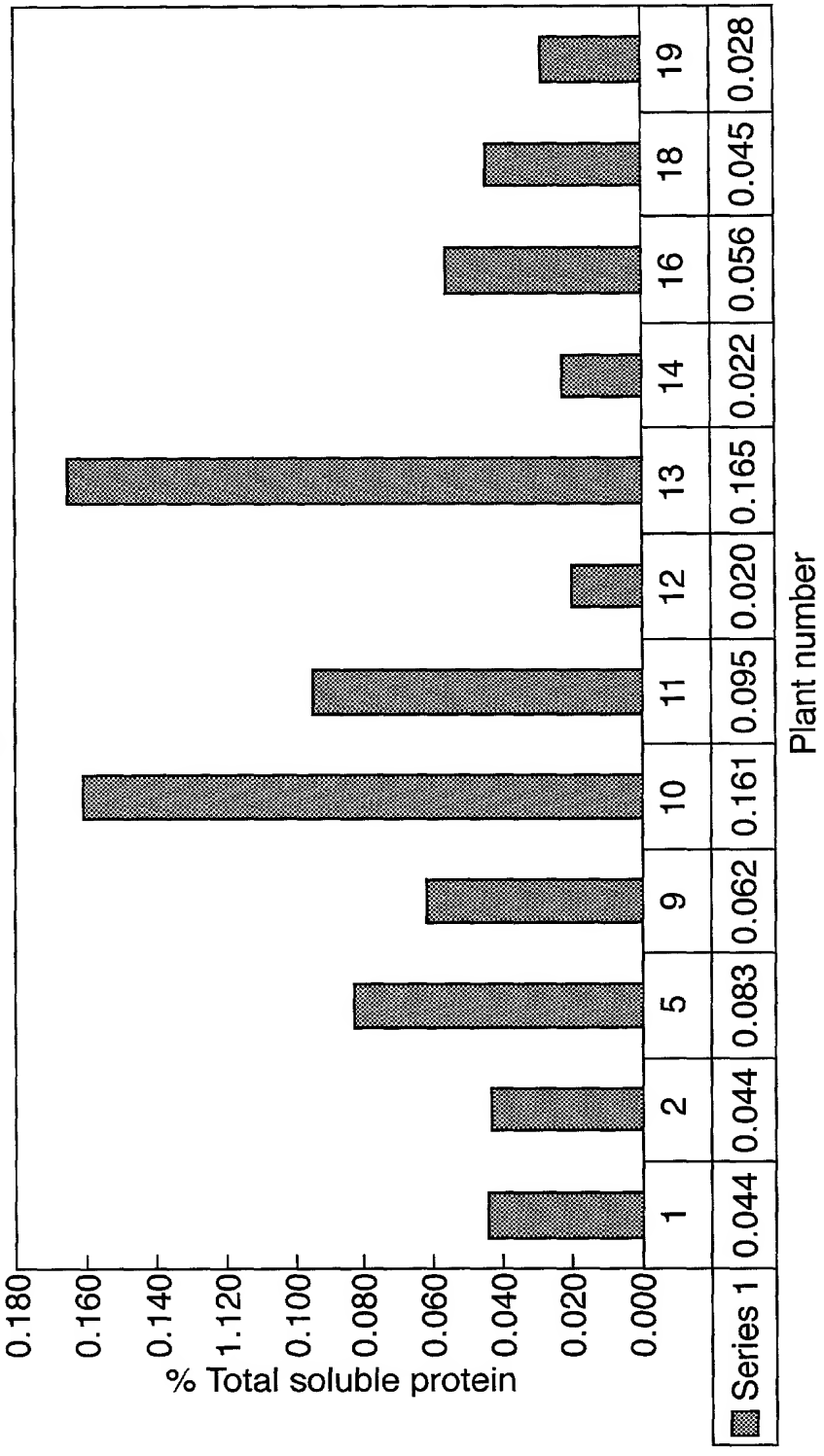
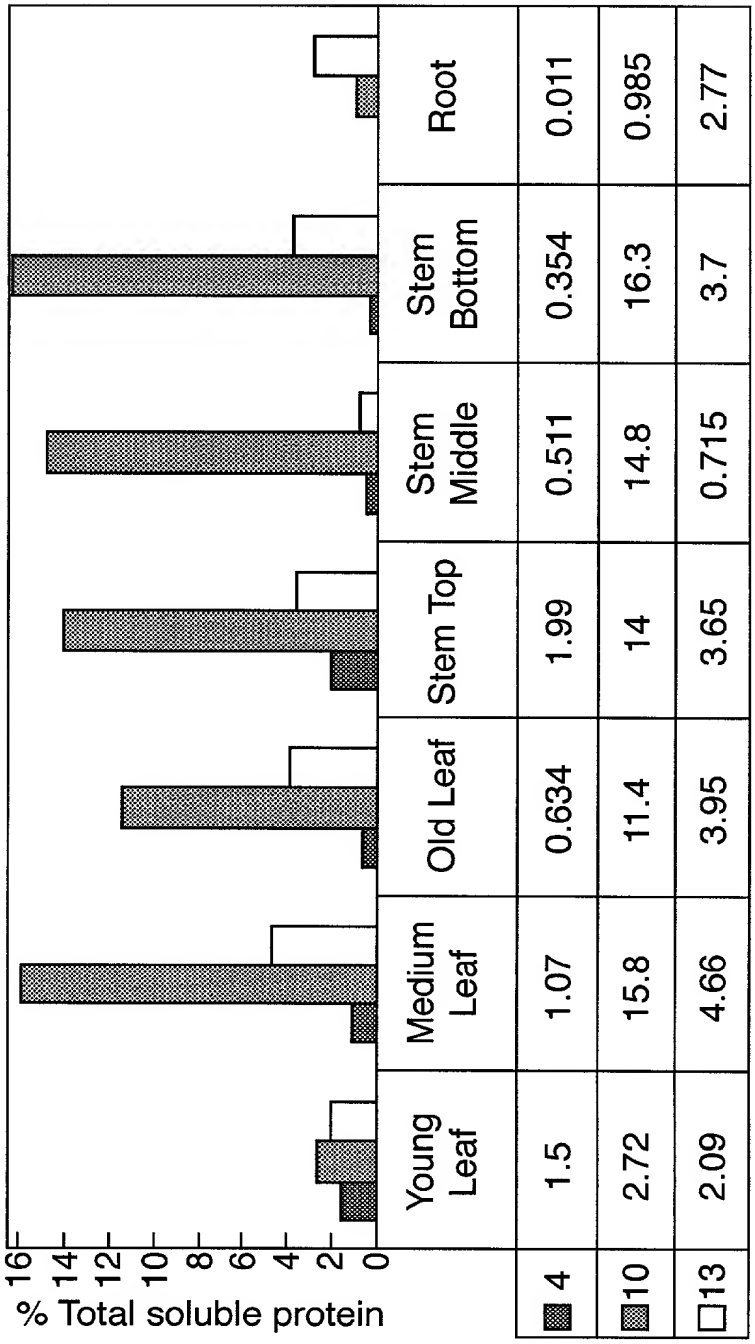
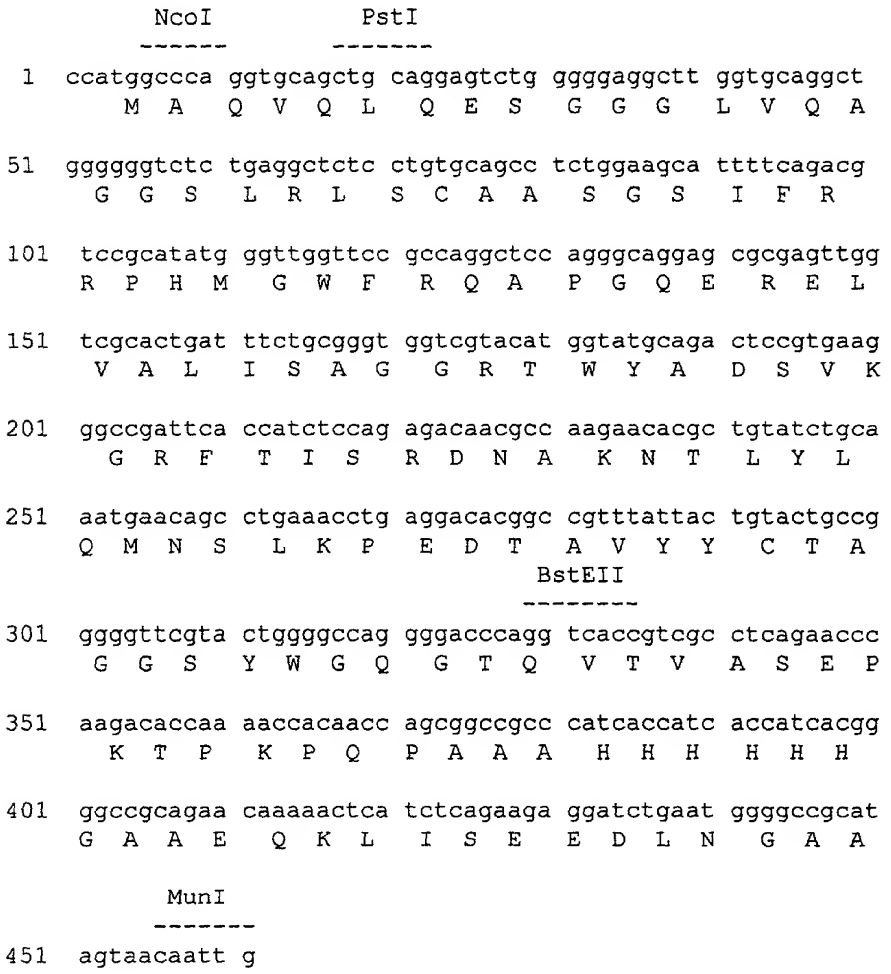

0.180
0.160
0.140
1.120
0.100
0.080
0.060
0.040
0.020
0.000
% Total soluble protein
Plant number
Series 1
1 0.044
2 0.044
5 0.083
9 0.062
10 0.161
11 0.095
12 0.020
13 0.165
14 0.022
16 0.056
18 0.045
19 0.028

Fig.27.



	Young Leaf	Medium Leaf	Old Leaf	Stem Top	Stem Middle	Stem Bottom	Root
4	1.5	1.07	0.634	1.99	0.511	0.354	0.011
10	2.72	15.8	11.4	14	14.8	16.3	0.985
13	2.09	4.66	3.95	3.65	0.715	3.7	2.77

Fig.28.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PstI
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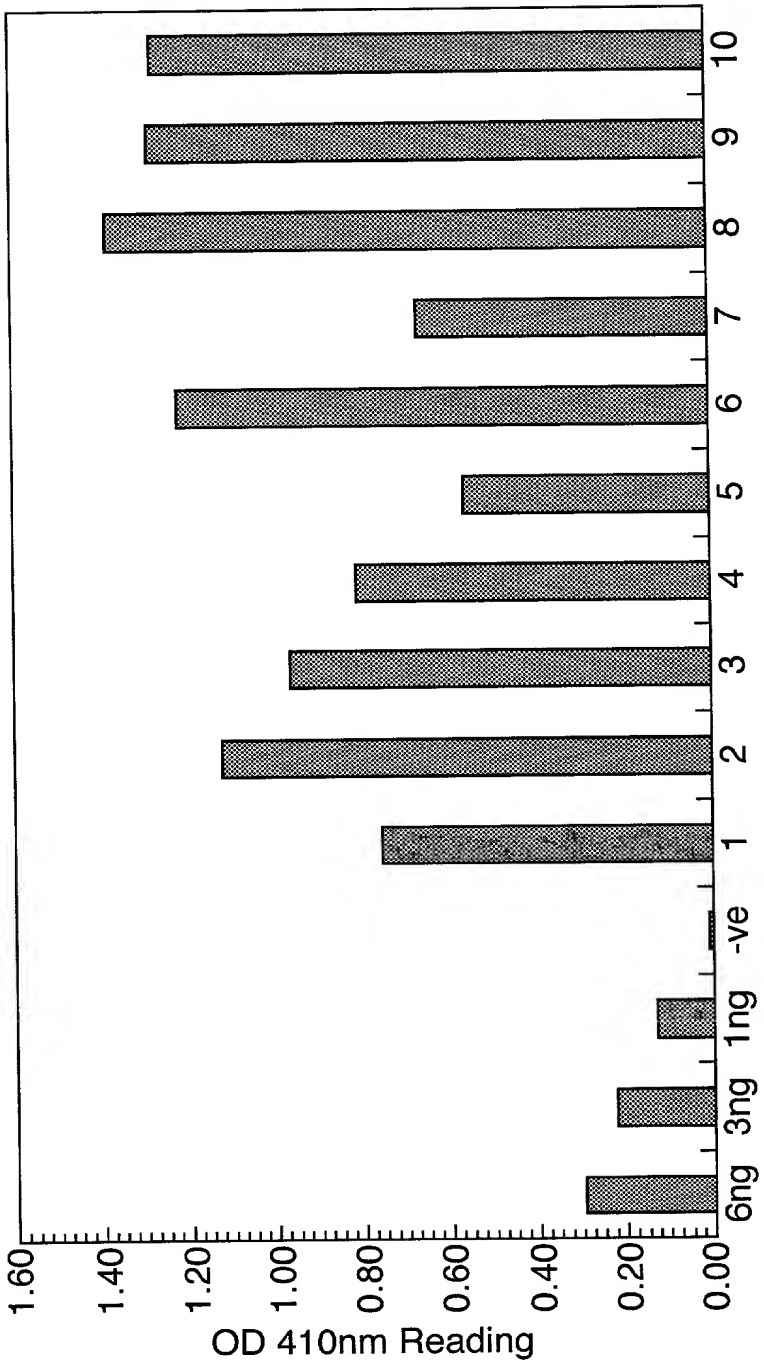
M A Q V Q L Q E S G G G L V Q A
51 gggggtctc tgaggctctc ctgtgcagcc tctggaagca ttttcagacg
G G S L R L S C A A S G S I F R
101 tccgcatatg ggttggttcc gccaggctcc agggcaggag cgcgagttgg
R P H M G W F R Q A P G Q E R E L
151 tcgcactgat ttctgcgggt ggtcgtacat ggtatgcaga ctccgtgaag
V A L I S A G G R T W Y A D S V K
201 ggccgattca ccatctccag agacaacgcc aagaacacgc tgtatctgca
G R F T I S R D N A K N T L Y L
251 aatgaacagc ctgaaacctg aggacacggc cgtttattac tgtactgccg
Q M N S L K P E D T A V Y Y C T A
BstEII
301 ggggttcgta ctggggccag gggacccagg tcaccgtcgc ctcagaaccc
G G S Y W G Q G T Q V T V A S E P
351 aagacaccaa aaccacaacc agcggccgcc catcaccatc accatcacgg
K T P K P Q P A A A H H H H H H
401 ggccgcagaa caaaaactca tctcagaaga ggatctgaat ggggccgcat
G A A E Q K L I S E E D L N G A A
MunI
451 agtaacaatt g

Fig.29.


1.60
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
OD 410nm Reading
6ng
3ng
1ng
-ve
1
2
3
4
5
6
7
8
9
10